SEQUENCE LISTING

<110> HE, STEVE S.
       DOTSON, STANTON B.

<120> NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL
       PROLIFERATION AND GROWTH AND USES THEREOF

<130> 16517.327

<140> 10/024,632
<141> 2001-12-19

<150> 60/257,896
<151> 2000-12-21

<160> 42

<170> PatentIn Ver. 3.3

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aactgctagc aatttcaaat cttttcgagt aaccaaaaag aaaaaaacaa aaagcaagaa 240

g atg aag cgc ata aat gag agt aac aac acc gat gat gga aac aat cat 289
  Met Lys Arg Ile Asn Glu Ser Asn Asn Thr Asp Asp Gly Asn Asn His
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aac tgg ttg ggg ttc tct ctc tca ccc cac atg aaa atg gag gct act 337
Asn Trp Leu Gly Phe Ser Leu Ser Pro His Met Lys Met Glu Ala Thr
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tca gca gcc act gtt ccg aca acc ttc tac atg tcc cct tct caa tct 385
Ser Ala Ala Thr Val Pro Thr Thr Phe Tyr Met Ser Pro Ser Gln Ser
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cac ttg tcc aac ttc gga atg tgt tac ggt gtc gga gaa aat ggt aac 433
His Leu Ser Asn Phe Gly Met Cys Tyr Gly Val Gly Glu Asn Gly Asn
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ttc cat tct cca ctt acg gtt atg cct ctc aag tct gat ggg tca ctt 481
Phe His Ser Pro Leu Thr Val Met Pro Leu Lys Ser Asp Gly Ser Leu
 65   70   75   80

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tgt atc ttg gaa gct ctc aaa aga tca caa acg caa gtg atg gtg cca    529
Cys Ile Leu Glu Ala Leu Lys Arg Ser Gln Thr Gln Val Met Val Pro
                85                  90                  95

act tcg tct ccg aaa ttg gag gac ttt cta ggt ggt gca act atg gga    577
Thr Ser Ser Pro Lys Leu Glu Asp Phe Leu Gly Gly Ala Thr Met Gly
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act cac gaa tat gga agc cac gag aga ggt ttg agc cta gac agc atc    625
Thr His Glu Tyr Gly Ser His Glu Arg Gly Leu Ser Leu Asp Ser Ile
                115                 120                 125

tat tat aac tcc caa aac gca gag gct caa ccc aac aga gac ctt ctt    673
Tyr Tyr Asn Ser Gln Asn Ala Glu Ala Gln Pro Asn Arg Asp Leu Leu
        130                 135                 140

tca caa ccc ttc agg caa caa ggt cat atg agt gtc caa aca cac cct    721
Ser Gln Pro Phe Arg Gln Gln Gly His Met Ser Val Gln Thr His Pro
145                 150                 155                 160

tat tac tca ggc ctt gct tgc cat ggt tta tat caa gca ccg ttg gag    769
Tyr Tyr Ser Gly Leu Ala Cys His Gly Leu Tyr Gln Ala Pro Leu Glu
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gaa gaa aca aca aag gaa acg cac gtg tcg gat tgc agc tcc cta atg    817
Glu Glu Thr Thr Lys Glu Thr His Val Ser Asp Cys Ser Ser Leu Met
                180                 185                 190

cct caa atg aca gaa ggc ttg aaa aac tgg gtg gct cca aca agg gag    865
Pro Gln Met Thr Glu Gly Leu Lys Asn Trp Val Ala Pro Thr Arg Glu
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ttt tca act cac cag cag gtt ttg gag cag caa atg aat tgt ggc atg    913
Phe Ser Thr His Gln Gln Val Leu Glu Gln Gln Met Asn Cys Gly Met
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ggg aat gag aga aat ggt gtg tct tta gga tct gtg ggg tgt gga gag    961
Gly Asn Glu Arg Asn Gly Val Ser Leu Gly Ser Val Gly Cys Gly Glu
225                 230                 235                 240

tta cag tct cta agc tta tct atg agt cct ggt tct cag tct agt tgt    1009
Leu Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser Cys
                245                 250                 255

gtc act gct cct tct gga aca gat tct gtt gct gtg gat gca aag aag    1057
Val Thr Ala Pro Ser Gly Thr Asp Ser Val Ala Val Asp Ala Lys Lys
                260                 265                 270

aga ggg cat gct aaa ctt ggt cag aag cag cct gtg cat aga aaa tct    1105
Arg Gly His Ala Lys Leu Gly Gln Lys Gln Pro Val His Arg Lys Ser
        275                 280                 285

atc gac aca ttt ggg caa aga acc tcg cag tat aga ggt gtc aca agg    1153
Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr Arg
        290                 295                 300
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cat aga tgg act ggt agg tat gaa gcg cat ttg tgg gat aat agt tgc    1201
His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys
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aag aag gaa ggg caa act agg aaa gga cga caa gtg tat ttg ggg ggt    1249
Lys Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly
                325             330                 335

tat gat atg gag gag aaa gct gca aga gcc tat gat ctc gcg gcc ctt    1297
Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu
            340             345                 350

aag tac tgg gga cct tca acg cat ata aac ttt tcg ata gag aat tac    1345
Lys Tyr Trp Gly Pro Ser Thr His Ile Asn Phe Ser Ile Glu Asn Tyr
        355             360                 365

caa gtt caa ctt gag gaa atg aag aac atg agc aga cag gaa tac gtt    1393
Gln Val Gln Leu Glu Glu Met Lys Asn Met Ser Arg Gln Glu Tyr Val
370             375             380

gca cac ttg aga aga aaa agc agc ggg ttt tct aga ggt gct tca ata    1441
Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile
385             390             395                 400

tac aga ggg gtc aca agg cat cac caa cat gga aga tgg caa gcg agg    1489
Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg
                405             410                 415

ata ggc aga gtt gct ggg aac aaa gac ctt tac ctt ggg acg ttc agc    1537
Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser
                420             425                 430

acc caa gag gaa gca gca gaa gca tac gat gta gcg gcg atc aaa ttt    1585
Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys Phe
        435             440                 445

cgc ggc gca aat gca gtc aca aac ttt gac att tca aga tac gat gtg    1633
Arg Gly Ala Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val
    450             455             460

gag aga atc atg gcc agt agc aat ctc ctc gct ggg gag ctt gca agg    1681
Glu Arg Ile Met Ala Ser Ser Asn Leu Leu Ala Gly Glu Leu Ala Arg
465             470             475                 480

cgt aag aaa gat aac gat cct aga aac aag gac ata gac tac aac aag    1729
Arg Lys Lys Asp Asn Asp Pro Arg Asn Lys Asp Ile Asp Tyr Asn Lys
            485             490                 495

agt gta gta aca agt gtg aac aat gag gaa acg gtt caa gtt caa gca    1777
Ser Val Val Thr Ser Val Asn Asn Glu Glu Thr Val Gln Val Gln Ala
            500             505                 510

gga aac aac aat aat gaa aac gac tca gag tgg aag atg gtt tta ttt    1825
Gly Asn Asn Asn Asn Glu Asn Asp Ser Glu Trp Lys Met Val Leu Phe
            515             520                 525
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aac cac cct tca cag cag caa cag gca aat ggc aat ggc agt gac caa   1873
Asn His Pro Ser Gln Gln Gln Gln Ala Asn Gly Asn Gly Ser Asp Gln
    530             535             540

aaa ata atg aac tgt gga aat tac aga aac agt gca ttt tct atg gcc   1921
Lys Ile Met Asn Cys Gly Asn Tyr Arg Asn Ser Ala Phe Ser Met Ala
545             550             555             560

cta caa gat ctt att ggg att gat tcg gtg ggt tct ggg cag cat aat   1969
Leu Gln Asp Leu Ile Gly Ile Asp Ser Val Gly Ser Gly Gln His Asn
            565             570             575

atg ctg gac gag tct agc aaa att ggg act cat ttt tca aac acg tca   2017
Met Leu Asp Glu Ser Ser Lys Ile Gly Thr His Phe Ser Asn Thr Ser
            580             585             590

tcg ctg gtg aca agt tta agc agc tca aga gag gct agt cct gag aaa   2065
Ser Leu Val Thr Ser Leu Ser Ser Ser Arg Glu Ala Ser Pro Glu Lys
            595             600             605

agg ggt ccc tcg ctt ctg ttc cca atg cct cca atg gaa aca aag att   2113
Arg Gly Pro Ser Leu Leu Phe Pro Met Pro Pro Met Glu Thr Lys Ile
    610             615             620

gtg aac ccc att ggt acc agt gtt acc tct tgg cta ccc tca cca acg   2161
Val Asn Pro Ile Gly Thr Ser Val Thr Ser Trp Leu Pro Ser Pro Thr
625             630             635             640

gtt caa atg agg cct tct cct gct atc tct ttg tct cac ttg cca gtt   2209
Val Gln Met Arg Pro Ser Pro Ala Ile Ser Leu Ser His Leu Pro Val
            645             650             655

ttt gct tct tgg act gat act taa atggagatag gcacggtcca tttttcatgt  2263
Phe Ala Ser Trp Thr Asp Thr
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tatgttatgt aactaaaatt tacttttttc cttcatcttt tatttctaat ttgatttcct 2323

aagtttaaaa aaaaaaaaaa a                                            2344
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            20              25                  30

Ser Ala Ala Thr Val Pro Thr Thr Phe Tyr Met Ser Pro Ser Gln Ser
        35              40                  45

His Leu Ser Asn Phe Gly Met Cys Tyr Gly Val Gly Glu Asn Gly Asn
    50              55                  60
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Phe His Ser Pro Leu Thr Val Met Pro Leu Lys Ser Asp Gly Ser Leu
65              70              75                      80

Cys Ile Leu Glu Ala Leu Lys Arg Ser Gln Thr Gln Val Met Val Pro
            85              90                      95

Thr Ser Ser Pro Lys Leu Glu Asp Phe Leu Gly Gly Ala Thr Met Gly
            100             105             110

Thr His Glu Tyr Gly Ser His Glu Arg Gly Leu Ser Leu Asp Ser Ile
        115             120             125

Tyr Tyr Asn Ser Gln Asn Ala Glu Ala Gln Pro Asn Arg Asp Leu Leu
    130             135             140

Ser Gln Pro Phe Arg Gln Gln Gly His Met Ser Val Gln Thr His Pro
145             150             155             160

Tyr Tyr Ser Gly Leu Ala Cys His Gly Leu Tyr Gln Ala Pro Leu Glu
            165             170             175

Glu Glu Thr Thr Lys Glu Thr His Val Ser Asp Cys Ser Ser Leu Met
        180             185             190

Pro Gln Met Thr Glu Gly Leu Lys Asn Trp Val Ala Pro Thr Arg Glu
        195             200             205

Phe Ser Thr His Gln Gln Val Leu Glu Gln Gln Met Asn Cys Gly Met
    210             215             220

Gly Asn Glu Arg Asn Gly Val Ser Leu Gly Ser Val Gly Cys Gly Glu
225             230             235             240

Leu Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser Cys
            245             250             255

Val Thr Ala Pro Ser Gly Thr Asp Ser Val Ala Val Asp Ala Lys Lys
            260             265             270

Arg Gly His Ala Lys Leu Gly Gln Lys Gln Pro Val His Arg Lys Ser
        275             280             285

Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr Arg
    290             295             300

His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys
305             310             315             320

Lys Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly
            325             330             335

Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu
        340             345             350

Lys Tyr Trp Gly Pro Ser Thr His Ile Asn Phe Ser Ile Glu Asn Tyr
        355             360             365
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Gln Val Gln Leu Glu Glu Met Lys Asn Met Ser Arg Gln Glu Tyr Val
370   375   380

Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile
385   390   395   400

Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg
405   410   415

Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser
420   425   430

Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys Phe
435   440   445

Arg Gly Ala Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val
450   455   460

Glu Arg Ile Met Ala Ser Ser Asn Leu Leu Ala Gly Glu Leu Ala Arg
465   470   475   480

Arg Lys Lys Asp Asn Asp Pro Arg Asn Lys Asp Ile Asp Tyr Asn Lys
485   490   495

Ser Val Val Thr Ser Val Asn Asn Glu Glu Thr Val Gln Val Gln Ala
500   505   510

Gly Asn Asn Asn Asn Glu Asn Asp Ser Glu Trp Lys Met Val Leu Phe
515   520   525

Asn His Pro Ser Gln Gln Gln Ala Asn Gly Asn Gly Ser Asp Gln
530   535   540

Lys Ile Met Asn Cys Gly Asn Tyr Arg Asn Ser Ala Phe Ser Met Ala
545   550   555   560

Leu Gln Asp Leu Ile Gly Ile Asp Ser Val Gly Ser Gly Gln His Asn
565   570   575

Met Leu Asp Glu Ser Ser Lys Ile Gly Thr His Phe Ser Asn Thr Ser
580   585   590

Ser Leu Val Thr Ser Leu Ser Ser Ser Arg Glu Ala Ser Pro Glu Lys
595   600   605

Arg Gly Pro Ser Leu Leu Phe Pro Met Pro Met Glu Thr Lys Ile
610   615   620

Val Asn Pro Ile Gly Thr Ser Val Thr Ser Trp Leu Pro Ser Pro Thr
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Val Gln Met Arg Pro Ser Pro Ala Ile Ser Leu Ser His Leu Pro Val
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Phe Ala Ser Trp Thr Asp Thr
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Ala Asp Leu Asn Asn Gln Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro
 10              15                  20                      25

caa atg cat aat ata gga gtt tct tca cac tca caa cct tcc tct gct      147
Gln Met His Asn Ile Gly Val Ser Ser His Ser Gln Pro Ser Ser Ala
                30                  35                      40

gct gaa gtg gtt cct aca agc ttt tac cac cac act gct cca ctt agt      195
Ala Glu Val Val Pro Thr Ser Phe Tyr His His Thr Ala Pro Leu Ser
            45                  50                  55

agc tat ggt ttc tac tat gga ctt gaa gct gaa aat gtt gga ttg tat      243
Ser Tyr Gly Phe Tyr Tyr Gly Leu Glu Ala Glu Asn Val Gly Leu Tyr
        60                  65                  70

tca gct ttg cca atc atg ccc ctc aaa tct gat ggc tct ctc tat gga      291
Ser Ala Leu Pro Ile Met Pro Leu Lys Ser Asp Gly Ser Leu Tyr Gly
    75                  80                  85

ttg gaa act tta agc agg tca caa gca caa gca atg gct act act tca      339
Leu Glu Thr Leu Ser Arg Ser Gln Ala Gln Ala Met Ala Thr Thr Ser
 90                  95                  100                 105

aca cca aaa ctg gag aac ttc tta ggt ggg gaa gcc atg ggg acc cct      387
Thr Pro Lys Leu Glu Asn Phe Leu Gly Gly Glu Ala Met Gly Thr Pro
                110                 115                 120

cat cac tac gaa tgt agt gcc aca gaa aca atg cct ctg agc tta gac      435
His His Tyr Glu Cys Ser Ala Thr Glu Thr Met Pro Leu Ser Leu Asp
                125                 130                 135

agt gtt ttt tac atc caa ccc tca cgc cgt gac cca aat aat aac caa      483
Ser Val Phe Tyr Ile Gln Pro Ser Arg Arg Asp Pro Asn Asn Asn Gln
            140                 145                 150

acc tac caa aac cat gtt caa cac att agc acc aac caa caa caa caa      531
Thr Tyr Gln Asn His Val Gln His Ile Ser Thr Asn Gln Gln Gln Gln
        155                 160                 165

cag caa gag ctt caa gca tat tac tct acc ttg aga aac cat gat atg      579
Gln Gln Glu Leu Gln Ala Tyr Tyr Ser Thr Leu Arg Asn His Asp Met
170                 175                 180                 185
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ata tta gaa ggg tca aag caa agc caa act tct gac aac aac aat ctt.   627
Ile Leu Glu Gly Ser Lys Gln Ser Gln Thr Ser Asp Asn Asn Asn Leu
            190             195             200

cat gtt caa aac atg ggt ggt gat gat gcc gtt cct gtt cct ggc ctc   675
His Val Gln Asn Met Gly Gly Asp Asp Ala Val Pro Val Pro Gly Leu
            205             210           .   215

aag agt tgg gaa gtg agg aac ttc caa gct agc cat gca cat gag tca   723
Lys Ser Trp Glu Val Arg Asn Phe Gln Ala Ser His Ala His Glu Ser
            220             225             230

aag atg att gtt cct cat gtg gag gaa aat gct ggt gaa tca ggg tcc   771
Lys Met Ile Val Pro His Val Glu Glu Asn Ala Gly Glu Ser Gly Ser
            235             240             245

att gga tca atg gct tat ggt gac ttg caa tcg ttg agc ttg tcc atg   819
Ile Gly Ser Met Ala Tyr Gly Asp Leu Gln Ser Leu Ser Leu Ser Met
250             255             260             265

agt cct agc tct cag tct agc agt gtc aca agt tct cac cgt gct tca   867
Ser Pro Ser Ser Gln Ser Ser Ser Val Thr Ser Ser His Arg Ala Ser
            270             275             280

cct gct gtc gtt gat tct gtt gcc atg gat act aag aaa agg ggg cct   915
Pro Ala Val Val Asp Ser Val Ala Met Asp Thr Lys Lys Arg Gly Pro
            285             290             295

gaa aag gtt gac cag aag caa att gtt cat agg aag tcc att gac acc   963
Glu Lys Val Asp Gln Lys Gln Ile Val His Arg Lys Ser Ile Asp Thr
            300             305             310

ttt gga caa aga acc tcc cag tat aga gga gta aca agg cat agg tgg   1011
Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp
            315             320             325

act ggg aga tat gaa gct cat ctt tgg gac aac agc tgc aag aaa gag   1059
Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Lys Lys Glu
330             335             340             345

ggg caa agc agg aaa gga aga caa gtt tat cta ggg ggt tat gat atg   1107
Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Met
            350             355             360   .

gaa gaa aaa gct gcg aga gct tat gat cta gcg gca ctc aag tat tgg   1155
Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
            365             370             375

gga ccc tcc act cac ata aac ttt cct ttg gaa aat tat caa aat gaa   1203
Gly Pro Ser Thr His Ile Asn Phe Pro Leu Glu Asn Tyr Gln Asn Glu
            380             385             390

ctt gag gaa atg aag aac atg act aga caa gag tat gtt gct cat ttg   1251
Leu Glu Glu Met Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu
            395             400             405
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aga aga aaa agc agc gga ttc tca aga ggg gct tcc atg tac aga gga    1299
Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg Gly
410             415             420             .   425

gta aca aga cac cac caa cat gga agg tgg caa gct cga att ggt aga    1347
Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
                430             435             440

gtg gct gga aac aaa gat cta tat ctt gga acc ttt agt aca caa gag    1395
Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu
                445             450             455

gaa gca gct gaa gcc tat gat att gct gct ata aaa ttc cga gga gcg    1443
Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Ala
            460             465             470

aat gct gta acc aac ttt gac atc aca aga tat gat gtg gag aaa atc    1491
Asn Ala Val Thr Asn Phe Asp Ile Thr Arg Tyr Asp Val Glu Lys Ile
            475             480             485

atg gca agc agc aac ctc ctt agc agt gag cta gct agg cgc aac cga    1539
Met Ala Ser Ser Asn Leu Leu Ser Ser Glu Leu Ala Arg Arg Asn Arg
490             495             500             505

gag acg gac aat gaa act cag tgc att gat caa aat cac aat aag cct    1587
Glu Thr Asp Asn Glu Thr Gln Cys Ile Asp Gln Asn His Asn Lys Pro
                510             515             520

tct gca tat gag gac act caa gaa gct att cta atg cac cag aag agc    1635
Ser Ala Tyr Glu Asp Thr Gln Glu Ala Ile Leu Met His Gln Lys Ser
                525             530             535

tgt gag agc gaa aat gat cag tgg aag atg gtt ctc tac caa tcc tct    1683
Cys Glu Ser Glu Asn Asp Gln Trp Lys Met Val Leu Tyr Gln Ser Ser
            540             545             550

cag caa ctt gag cag aat cca cca aca att gag agt gac aga act aac    1731
Gln Gln Leu Glu Gln Asn Pro Pro Thr Ile Glu Ser Asp Arg Thr Asn
            555             560             565

cag tcc ttc gca gtg gct ttg gac aac atg ttt cat cag gaa gta gag    1779
Gln Ser Phe Ala Val Ala Leu Asp Asn Met Phe His Gln Glu Val Glu
570             575             580             585

gaa tca agt aag gcg agg acg cat gtg tca aat cct tct tca ttg gcc    1827
Glu Ser Ser Lys Ala Arg Thr His Val Ser Asn Pro Ser Ser Leu Ala
                590             595             600

aca agt ttg agc agc tca aga gaa ggt agc cct gat agg aca agc ttg    1875
Thr Ser Leu Ser Ser Ser Arg Glu Gly Ser Pro Asp Arg Thr Ser Leu
                605             610             615

cca atg ctc tct gga atg cct tca act gca tca aaa cta ttg gct act    1923
Pro Met Leu Ser Gly Met Pro Ser Thr Ala Ser Lys Leu Leu Ala Thr
        620             625             630
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aat cca aat aac gtg aat tct tgg gac cct tca ccc cat ttg agg cca   1971
Asn Pro Asn Asn Val Asn Ser Trp Asp Pro Ser Pro His Leu Arg Pro
    635             640             645

gca ctt act ttg cct caa atg cca gtt ttt gca gct tgg aca gat gca   2019
Ala Leu Thr Leu Pro Gln Met Pro Val Phe Ala Ala Trp Thr Asp Ala
650             655             660             665

tag ttcatagctc aatagtcctt ttaatttttt gttctctcaa gtgaaatttc        2072


aatccttttt attgtctttt tttgcatgca tgaacaacac aagaggaagg ggttgtagct 2132

agtcaaatgg agggtctaaa tattatatca tcacatcact gtcagcaagt ttaatttaaa 2192

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            20                  25                  30

Ser Ser His Ser Gln Pro Ser Ser Ala Ala Glu Val Val Pro Thr Ser
        35                  40                  45

Phe Tyr His His Thr Ala Pro Leu Ser Ser Tyr Gly Phe Tyr Tyr Gly
    50                  55                  60

Leu Glu Ala Glu Asn Val Gly Leu Tyr Ser Ala Leu Pro Ile Met Pro
65                  70                  75                  80

Leu Lys Ser Asp Gly Ser Leu Tyr Gly Leu Glu Thr Leu Ser Arg Ser
                85                  90                  95

Gln Ala Gln Ala Met Ala Thr Thr Ser Thr Pro Lys Leu Glu Asn Phe
            100                 105                 110

Leu Gly Gly Glu Ala Met Gly Thr Pro His His Tyr Glu Cys Ser Ala
            115                 120                 125

Thr Glu Thr Met Pro Leu Ser Leu Asp Ser Val Phe Tyr Ile Gln Pro
    130                 135                 140

Ser Arg Arg Asp Pro Asn Asn Asn Gln Thr Tyr Gln Asn His Val Gln
145                 150                 155                 160
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His Ile Ser Thr Asn Gln Gln Gln Gln Gln Glu Leu Gln Ala Tyr
            165   170   175

Tyr Ser Thr Leu Arg Asn His Asp Met Ile Leu Glu Gly Ser Lys Gln
            180   185   190

Ser Gln Thr Ser Asp Asn Asn Asn Leu His Val Gln Asn Met Gly Gly
        195   200   205

Asp Asp Ala Val Pro Val Pro Gly Leu Lys Ser Trp Glu Val Arg Asn
    210   215   220

Phe Gln Ala Ser His Ala His Glu Ser Lys Met Ile Val Pro His Val
225   230   235   240

Glu Glu Asn Ala Gly Glu Ser Gly Ser Ile Gly Ser Met Ala Tyr Gly
            245   250   255

Asp Leu Gln Ser Leu Ser Leu Ser Met Ser Pro Ser Ser Gln Ser Ser
        260   265   270

Ser Val Thr Ser Ser His Arg Ala Ser Pro Ala Val Val Asp Ser Val
        275   280   285

Ala Met Asp Thr Lys Lys Arg Gly Pro Glu Lys Val Asp Gln Lys Gln
    290   295   300

Ile Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln
305   310   315   320

Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His
            325   330   335

Leu Trp Asp Asn Ser Cys Lys Lys Glu Gly Gln Ser Arg Lys Gly Arg
  ·   340   345   350

Gln Val Tyr Leu Gly Gly Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala
        355   360   365

Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr His Ile Asn
    370   375   380

Phe Pro Leu Glu Asn Tyr Gln Asn Glu Leu Glu Glu Met Lys Asn Met
385   390   395   400

Thr Arg Gln Glu Tyr Val Ala His Leu Arg Arg Lys Ser Ser Gly Phe
            405   410   415

Ser Arg Gly Ala Ser Met Tyr Arg Gly Val Thr Arg His His Gln His
        420   425   430

Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu
        435   440   445

Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp
    450   455   460

Ile Ala Ala Ile Lys Phe Arg Gly Ala Asn Ala Val Thr Asn Phe Asp
465   470   475   480

Ile Thr Arg Tyr Asp Val Glu Lys Ile Met Ala Ser Ser Asn Leu Leu
            485   490   495

Ser Ser Glu Leu Ala Arg Arg Asn Arg Glu Thr Asp Asn Glu Thr Gln
        500   505   510

Cys Ile Asp Gln Asn His Asn Lys Pro Ser Ala Tyr Glu Asp Thr Gln
        515   520   525

Glu Ala Ile Leu Met His Gln Lys Ser Cys Glu Ser Glu Asn Asp Gln
        530   535   540

Trp Lys Met Val Leu Tyr Gln Ser Ser Gln Gln Leu Glu Gln Asn Pro
545   550   555   560

Pro Thr Ile Glu Ser Asp Arg Thr Asn Gln Ser Phe Ala Val Ala Leu
            565   570   575

Asp Asn Met Phe His Gln Glu Val Glu Glu Ser Ser Lys Ala Arg Thr
        580   585   590

His Val Ser Asn Pro Ser Ser Leu Ala Thr Ser Leu Ser Ser Ser Arg
        595   600   605

Glu Gly Ser Pro Asp Arg Thr Ser Leu Pro Met Leu Ser Gly Met Pro
    610   615   620

Ser Thr Ala Ser Lys Leu Leu Ala Thr Asn Pro Asn Asn Val Asn Ser
625   630   635   640

Trp Asp Pro Ser Pro His Leu Arg Pro Ala Leu Thr Leu Pro Gln Met
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Pro Val Phe Ala Ala Trp Thr Asp Ala
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ccg cac atg ccg gcc atg gag gtg ccg tcc tcc tct gag cca tcg act    96
Pro His Met Pro Ala Met Glu Val Pro Ser Ser Ser Glu Pro Ser Thr
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gct gct cat cat cat cat cat cat cat cca cct gct gct gct gct gct   144
Ala Ala His His His His His His His Pro Pro Ala Ala Ala Ala Ala
            35                  40              45

gcc gga gcc atg tcg tct cct ccc gac agc gcc acg acc tgc aac ttc   192
Ala Gly Ala Met Ser Ser Pro Pro Asp Ser Ala Thr Thr Cys Asn Phe
        50              55              60

ctc ttc tcc cct cct gca gca cag atg gtc gct cct tca cct ggc tac   240
Leu Phe Ser Pro Pro Ala Ala Gln Met Val Ala Pro Ser Pro Gly Tyr
65              70              75              80

tac tac gtc ggc ggc gcc tac gga gac ggg acc agc acc gcc ggc gtc   288
Tyr Tyr Val Gly Gly Ala Tyr Gly Asp Gly Thr Ser Thr Ala Gly Val
            85                  90              95

tac tac tcg cac ctc cct gtc atg cct atc aag tcc gat ggc tcc ctc   336
Tyr Tyr Ser His Leu Pro Val Met Pro Ile Lys Ser Asp Gly Ser Leu
            100                 105             110

tgc atc atg gaa ggc atg atg ccg tcg tca tcg cca aag ctc gag gac   384
Cys Ile Met Glu Gly Met Met Pro Ser Ser Ser Pro Lys Leu Glu Asp
        115                 120             125

ttc ttg ggg tgt ggc aat ggc agt ggc cat gac ccg gcc acc tac tat   432
Phe Leu Gly Cys Gly Asn Gly Ser Gly His Asp Pro Ala Thr Tyr Tyr
    130                 135             140

agc cag ggc caa gaa gca gag gat gca agc agg gcg gcc tac cag cac   480
Ser Gln Gly Gln Glu Ala Glu Asp Ala Ser Arg Ala Ala Tyr Gln His
145                 150             155             160

cac cag cta gtc ccc tac aac tac cag cca ttg acg gaa gca gag atg   528
His Gln Leu Val Pro Tyr Asn Tyr Gln Pro Leu Thr Glu Ala Glu Met
                165             170             175

ctg caa gag gcc gca gcg gcg cca atg gag gac gca atg gcg gcg gcc   576
Leu Gln Glu Ala Ala Ala Ala Pro Met Glu Asp Ala Met Ala Ala Ala
            180             185             190

aag aac ttc ctc gtc acc agc tac ggc gcc tgc tac ggc aac cag gag   624
Lys Asn Phe Leu Val Thr Ser Tyr Gly Ala Cys Tyr Gly Asn Gln Glu
            195             200             205

atg ccg cag ccg ctc agc ctc tcc atg agc cca ggg tcc cag tcc agc   672
Met Pro Gln Pro Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser
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agc tgc gtc agt gca gct ccc cag cag cat cag cag atg gcg gtg gtc   720
Ser Cys Val Ser Ala Ala Pro Gln Gln His Gln Gln Met Ala Val Val
225             230             235             240
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gct gca gct gct gct gct ggt gat ggc cag gga agc aac agt aat gac    768
Ala Ala Ala Ala Ala Ala Gly Asp Gly Gln Gly Ser Asn Ser Asn Asp
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ggt ggc gag cag cgt gtc ggg aag aag agg ggc acc ggg aaa ggg ggc    816
Gly Gly Glu Gln Arg Val Gly Lys Lys Arg Gly Thr Gly Lys Gly Gly
                  260                 265                 270

caa aag cag cct gtt cac cgg aag tcc att gac acg ttt ggg cag agg    864
Gln Lys Gln Pro Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg
              275                 280                 285

aca tcg cag tat agg ggc gtc acc agg cac agg tgg act gga aga tat    912
Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
          290                 295                 300

gaa gcc cac ctc tgg gat aac agt tgc aaa aag gat gga cag aca agg    960
Glu Ala His Leu Trp Asp Asn Ser Cys Lys Lys Asp Gly Gln Thr Arg
305                 310                 315                 320

aag gga agg caa gta tat cta ggt ggt tat gac act gaa gat aaa gct   1008
Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Thr Glu Asp Lys Ala
                  325                 330                 335

gcg agg gct tat gat ctg gct gcg ctg aaa tac tgg ggg cta tct acg   1056
Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Leu Ser Thr
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cat ata aat ttc ccg tta gaa aac tac cga gat gag atc gag gag atg   1104
His Ile Asn Phe Pro Leu Glu Asn Tyr Arg Asp Glu Ile Glu Glu Met
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gaa agg atg aca agg caa gaa tat gtt gcg cac ttg aga agg aga agc   1152
Glu Arg Met Thr Arg Gln Glu Tyr Val Ala His Leu Arg Arg Arg Ser
          370                 375                 380

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Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His
385                 390                 395                 400

cac cag cat gga aga tgg caa gct cgg att ggc agg gtt gct ggc aac   1248
His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn
                  405                 410                 415

aag gac ttg tat ctc ggc act ttc agc act caa gaa gaa gca gca gag   1296
Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu
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gca tac gac att gct gcc atc aag ttc cgt ggc ctg aac gcg gtg acg   1344
Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr
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aac ttt gac atc aca agg tac gac gtg gac aag atc atg gag agc agc   1392
Asn Phe Asp Ile Thr Arg Tyr Asp Val Asp Lys Ile Met Glu Ser Ser
450                 455                 460
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465             470             475                 480

gcg ccg gac cat gtg cca ata ggc cgc gag ctc ggt gcg acc gag gaa      1488
Ala Pro Asp His Val Pro Ile Gly Arg Glu Leu Gly Ala Thr Glu Glu
                485             490   .           495

gcg agc gct gct act gtc acg ggc acc gac tgg aga atg gtg ctc cat      1536
Ala Ser Ala Ala Thr Val Thr Gly Thr Asp Trp Arg Met Val Leu His
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gga tca cag cag cag caa gct gca gcg tgc acc gaa gca acg gca gat      1584
Gly Ser Gln Gln Gln Gln Ala Ala Ala Cys Thr Glu Ala Thr Ala Asp
        515             520             525

ctt cag aag ggc ttc atg ggt gac gcg cac tcg gct ctc cac ggc att      1632
Leu Gln Lys Gly Phe Met Gly Asp Ala His Ser Ala Leu His Gly Ile
        530             535             540

gtc ggg ttc gac gtc gag tcg gcg gca gct gac gag atc gat gtc ccg      1680
Val Gly Phe Asp Val Glu Ser Ala Ala Ala Asp Glu Ile Asp Val Pro
545             550             555                 560

gga ggg aag atc agt ggc atc aac ttc tcg aac tcg tct tcg ctg gtg      1728
Gly Gly Lys Ile Ser Gly Ile Asn Phe Ser Asn Ser Ser Ser Leu Val
                565             570             575

act agc ctg agc aac tcg agg gag ggg agc cct gag agg ctt ggc ctc      1776
Thr Ser Leu Ser Asn Ser Arg Glu Gly Ser Pro Glu Arg Leu Gly Leu
                580             585             590

gcc atg ctc tac gcc aag cat cat ccc acc gcc gtc agc ctc gcc gcc      1824
Ala Met Leu Tyr Ala Lys His His Pro Thr Ala Val Ser Leu Ala Ala
        595             600             605

atg aac ccc tgg atg ccg atg ccg gcg ccg gcc gca gct cac gtg atg      1872
Met Asn Pro Trp Met Pro Met Pro Ala Pro Ala Ala Ala His Val Met
        610             615             620

agg ccg ccg agt gcc att gct cat ctc cct gtt ttt gca gcc tgg aca      1920
Arg Pro Pro Ser Ala Ile Ala His Leu Pro Val Phe Ala Ala Trp Thr
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gat gcc                                                               1926
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Ala Gly Ala Met Ser Ser Pro Pro Asp Ser Ala Thr Thr Cys Asn Phe
    50              55                  60

Leu Phe Ser Pro Pro Ala Ala Gln Met Val Ala Pro Ser Pro Gly Tyr
65              70                  75                      80

Tyr Tyr Val Gly Gly Ala Tyr Gly Asp Gly Thr Ser Thr Ala Gly Val
                85                  90                  95

Tyr Tyr Ser His Leu Pro Val Met Pro Ile Lys Ser Asp Gly Ser Leu
            100                 105                 110

Cys Ile Met Glu Gly Met Met Pro Ser Ser Ser Pro Lys Leu Glu Asp
        115                 120                 125

Phe Leu Gly Cys Gly Asn Gly Ser Gly His Asp Pro Ala Thr Tyr Tyr
    130                 135                 140

Ser Gln Gly Gln Glu Ala Glu Asp Ala Ser Arg Ala Ala Tyr Gln His
145                 150                 155                 160

His Gln Leu Val Pro Tyr Asn Tyr Gln Pro Leu Thr Glu Ala Glu Met
            165                 170                 175

Leu Gln Glu Ala Ala Ala Ala Pro Met Glu Asp Ala Met Ala Ala Ala
            180                 185                 190

Lys Asn Phe Leu Val Thr Ser Tyr Gly Ala Cys Tyr Gly Asn Gln Glu
        195                 200                 205

Met Pro Gln Pro Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser
    210                 215                 220

Ser Cys Val Ser Ala Ala Pro Gln Gln His Gln Gln Met Ala Val Val
225                 230                 235                 240

Ala Ala Ala Ala Ala Ala Gly Asp Gly Gln Gly Ser Asn Ser Asn Asp
                245                 250                 255

Gly Gly Glu Gln Arg Val Gly Lys Lys Arg Gly Thr Gly Lys Gly Gly
            260                 265                 270

Gln Lys Gln Pro Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg
        275                 280                 285

Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
    290                 295                 300

Glu Ala His Leu Trp Asp Asn Ser Cys Lys Lys Asp Gly Gln Thr Arg
305                 310                 315                 320
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Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Thr Glu Asp Lys Ala
            325   330   335

Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Leu Ser Thr
            340   345   350

His Ile Asn Phe Pro Leu Glu Asn Tyr Arg Asp Glu Ile Glu Glu Met
            355   360   365

Glu Arg Met Thr Arg Gln Glu Tyr Val Ala His Leu Arg Arg Arg Ser
    370   375   380

Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His
385   390   395   400

His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn
            405   410   415

Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu
            420   425   430

Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr
        435   440   445

Asn Phe Asp Ile Thr Arg Tyr Asp Val Asp Lys Ile Met Glu Ser Ser
    450   455   460

Ser Leu Leu Pro Gly Glu Ala Ala Arg Lys Val Lys Ala Ile Glu Ala
465   470   475   480

Ala Pro Asp His Val Pro Ile Gly Arg Glu Leu Gly Ala Thr Glu Glu
            485   490   495

Ala Ser Ala Ala Thr Val Thr Gly Thr Asp Trp Arg Met Val Leu His
        500   505   510

Gly Ser Gln Gln Gln Ala Ala Ala Cys Thr Glu Ala Thr Ala Asp
    515   520   525

Leu Gln Lys Gly Phe Met Gly Asp Ala His Ser Ala Leu His Gly Ile
    530   535   540

Val Gly Phe Asp Val Glu Ser Ala Ala Ala Asp Glu Ile Asp Val Pro
545   550   555   560

Gly Gly Lys Ile Ser Gly Ile Asn Phe Ser Asn Ser Ser Ser Leu Val
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Thr Ser Leu Ser Asn Ser Arg Glu Gly Ser Pro Glu Arg Leu Gly Leu
            580   585   590

Ala Met Leu Tyr Ala Lys His His Pro Thr Ala Val Ser Leu Ala Ala
    595   600   605

Met Asn Pro Trp Met Pro Met Pro Ala Pro Ala Ala Ala His Val Met
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Asp Ala

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caaaaaaaac tgacagtttt aaggttacaa ttttgtcaga attttatctt ttttgttatt 6240
ctctatgtag aatgaatttg aagatgcgac tttgcatgta gatgtaaatac tattgaaagt 6300
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agaatatgta aagtgtaaaa tgcttgccgg attcatgtgg attgaatgtt actgacttat 6660
ggacttcagt aaaccatgtc tttatgtggt tcttttctca tttacttagc aagaacagct 6720
gtgaccgtgc acattatcat gtatgttcat attatgaatt ggtggagtga aacttaaaaa 6780
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gattatatct tttttattcat tataattaaa ttttttataaa aagatctcac atgattttt 7260
tataatttaa tcacatgatg ttaactattg aaacatcgta taatatttac tgaaacatat 7320
gaataatact atgtgcaaca ttttttaatta actagtaaat acttgtt            7367
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<210> 8
<211> 2010
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (1)..(2010)

<400> 8
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atg gcc agt ggc aac agc agc agc agc agc ggc agc atg gct gcc acc    48
Met Ala Ser Gly Asn Ser Ser Ser Ser Ser Gly Ser Met Ala Ala Thr
 1               5                  10                  15

gcc gga ggt gtc ggc ggc tgg ctg gga ttc tcg ctg tcg ccg cac atg    96
Ala Gly Gly Val Gly Gly Trp Leu Gly Phe Ser Leu Ser Pro His Met
             20                  25                  30

gcg acg tac tgc gcc ggc ggc gtc gac gat gtc ggc cac cac cac cac   144
Ala Thr Tyr Cys Ala Gly Gly Val Asp Asp Val Gly His His His His
         35                  40                  45

cac cac gtg cac cag cat cag cag cag cat gga ggt ggg ctg ttc tac   192
His His Val His Gln His Gln Gln Gln His Gly Gly Gly Leu Phe Tyr
     50                  55                  60

aac cct gcc gcc gtc gcc tcc tcc ttc tac tac ggc ggc ggg cat gac   240
Asn Pro Ala Ala Val Ala Ser Ser Phe Tyr Tyr Gly Gly Gly His Asp
 65                  70                  75                  80

gcc gtc gtc acc tcc gcg gcc ggc ggc gga tcg tac tat ggc gcc ggg   288
Ala Val Val Thr Ser Ala Ala Gly Gly Gly Ser Tyr Tyr Gly Ala Gly
                 85                  90                  95
```

```
ttc tcc tcc atg ccg ctc aag tcc gac ggc tcg ctc tgc atc atg gag      336
Phe Ser Ser Met Pro Leu Lys Ser Asp Gly Ser Leu Cys Ile Met Glu
            100                 105                 110

gca ctc cgg gga ggc gac caa gaa cag caa ggg gtg gtg gtg tcg gcg      384
Ala Leu Arg Gly Gly Asp Gln Glu Gln Gln Gly Val Val Val Ser Ala
            115                 120                 125

tcg ccc aag ctg gag gat ttc cta ggc gcg ggc ccc gcc atg gcg ctg      432
Ser Pro Lys Leu Glu Asp Phe Leu Gly Ala Gly Pro Ala Met Ala Leu
            130                 135                 140

agc ctg gac aac tcc gcc ttc tac tac ggc ggc cac ggt cac cac cag      480
Ser Leu Asp Asn Ser Ala Phe Tyr Tyr Gly Gly His Gly His His Gln
145                 150                 155                 160

gga cac gcc cag gac ggc ggc gcc gtc ggt ggc gac ccg cac cac ggc      528
Gly His Ala Gln Asp Gly Gly Ala Val Gly Gly Asp Pro His His Gly
                165                 170                 175

ggc ggc ggc ttc ctg cag tgc gct gtc atc ccc ggc gcc ggc gcc ggc      576
Gly Gly Gly Phe Leu Gln Cys Ala Val Ile Pro Gly Ala Gly Ala Gly
            180                 185                 190

cac gac gcg gcg ctg gtg cac gac cag tcc gcc gcg gca gtg gcg gcc      624
His Asp Ala Ala Leu Val His Asp Gln Ser Ala Ala Ala Val Ala Ala
            195                 200                 205

ggc tgg gcg gcg atg cac ggc ggc ggc tac gac atc gcc aac gcc gcc      672
Gly Trp Ala Ala Met His Gly Gly Gly Tyr Asp Ile Ala Asn Ala Ala
            210                 215                 220

gcc gac gac gtc tgc gcc gcc ggc ccc atc atc ccc acc ggc ggc cac      720
Ala Asp Asp Val Cys Ala Ala Gly Pro Ile Ile Pro Thr Gly Gly His
225                 230                 235                 240

ctg cac cct ctc acc ctg tcc atg agc tcg gcc ggg tcc cag tcc agc      768
Leu His Pro Leu Thr Leu Ser Met Ser Ser Ala Gly Ser Gln Ser Ser
                245                 250                 255

tgc gtc acc gtg cag gcc gcc gcc gcc ggc gag ccg tac atg gcc atg      816
Cys Val Thr Val Gln Ala Ala Ala Ala Gly Glu Pro Tyr Met Ala Met
                260                 265                 270

gac gcc gtg agc aag aag cgc ggc ggc gcg gac cgc gcc ggg cag aag      864
Asp Ala Val Ser Lys Lys Arg Gly Gly Ala Asp Arg Ala Gly Gln Lys
            275                 280                 285

cag ccg gtg cac cgc aag tcc att gac acg ttc ggc cag agg acg tcg      912
Gln Pro Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser
            290                 295                 300

cag tac aga ggc gtc acc agg cat agg tgg act ggg aga tat gag gca      960
Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala
305                 310                 315                 320
```

```
cac ctc tgg gac aac agc tgc aag aag gaa ggc cag acc aga aaa gga    1008
His Leu Trp Asp Asn Ser Cys Lys Lys Glu Gly Gln Thr Arg Lys Gly
                325                 330                 335


cgc caa gtg tat ctt ggt ggg tat gac atg gag gag aag gct gcc agg    1056
Arg Gln Val Tyr Leu Gly Gly Tyr Asp Met Glu Glu Lys Ala Ala Arg
                340                 345                 350


gcg tat gat ctt gct gcg ctc aag tac tgg ggc cct tcc acg cac atc    1104
Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr His Ile
                355                 360                 365


aac ttc ccg ttg gag gac tac cag gag gag ctg gag gag atg aag aac    1152
Asn Phe Pro Leu Glu Asp Tyr Gln Glu Glu Leu Glu Glu Met Lys Asn
        370                 375                 380


atg agc agg cag gag tat gtg gct cac ctc aga agg aaa agc agt ggc    1200
Met Ser Arg Gln Glu Tyr Val Ala His Leu Arg Arg Lys Ser Ser Gly
385                 390                 395                 400


ttc tcg cgt ggc gct tcg atc tac cgt gga gtc acc agg cat cat cag    1248
Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln
                405                 410                 415


cac ggg aga tgg cag gcg cga atc ggc cgc gtc tcg ggc aac aag gac    1296
His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ser Gly Asn Lys Asp
                420                 425                 430


ctt tac ttg ggg aca ttc atc gcg tcg gct ttt gcc gcg gcg cgg cgc    1344
Leu Tyr Leu Gly Thr Phe Ile Ala Ser Ala Phe Ala Ala Ala Arg Arg
                435                 440                 445


gcg cgc cat gcc ggc acg cag gag gag gcg gcg gag gcg tac gac gtg    1392
Ala Arg His Ala Gly Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val
                450                 455                 460


gcg gcg atc aag ttc cgg ggg ctc aac gcc gtc acc aac ttc gac atc    1440
Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile
465                 470                 475                 480


acg agg tac gac gtg gac aag atc ctg gag agc agc acg ctc ctc ccg    1488
Thr Arg Tyr Asp Val Asp Lys Ile Leu Glu Ser Ser Thr Leu Leu Pro
                485                 490                 495


ggg gag ctg gcg cgg cgc aag ggt aag gtc ggc gac ggc ggc ggc gcg    1536
Gly Glu Leu Ala Arg Arg Lys Gly Lys Val Gly Asp Gly Gly Gly Ala
                500                 505                 510


gcg gcg gtc gcc gac gcc gcg gcc gcc ttg gtg cag gcc ggg aac gtg    1584
Ala Ala Val Ala Asp Ala Ala Ala Ala Leu Val Gln Ala Gly Asn Val
                515                 520                 525


gcg gag tgg aag atg gcc acc gcc gcc gcg ctg cca gcg gcg gcg aga    1632
Ala Glu Trp Lys Met Ala Thr Ala Ala Ala Leu Pro Ala Ala Ala Arg
        530                 535                 540
```

```
acg gag cag cag cag cag cat ggg cac ggc ggc cac caa cac cat gac    1680
Thr Glu Gln Gln Gln Gln His Gly His Gly Gly His Gln His His Asp
545             550             555             560

ctc ctg ccg agc gac gcc ttc tcg gtg ctg cag gac atc gtg tcg acc    1728
Leu Leu Pro Ser Asp Ala Phe Ser Val Leu Gln Asp Ile Val Ser Thr
            565             570             575

gtg gac gcg gcg ggc gcg ccg ccg cgc gcg ccg cac atg tcg atg gcg    1776
Val Asp Ala Ala Gly Ala Pro Pro Arg Ala Pro His Met Ser Met Ala
            580             585             590

gcg acg agc ctg ggc aac tcc cgg gag cag agc cct gac agg ggc gtc    1824
Ala Thr Ser Leu Gly Asn Ser Arg Glu Gln Ser Pro Asp Arg Gly Val
            595             600             605

ggc ggc ggc ggc ggc ggc ggc gtc ctc gcc acg ctg ttc gcc aag ccc    1872
Gly Gly Gly Gly Gly Gly Gly Val Leu Ala Thr Leu Phe Ala Lys Pro
    610             615             620

gcg gcg gcg tcg aag ctg tac agc ccg gtg ccg ctg aac acc tgg gcc    1920
Ala Ala Ala Ser Lys Leu Tyr Ser Pro Val Pro Leu Asn Thr Trp Ala
625             630             635             640

tcg ccc tcg ccg gcg gtg agc tcg gtg ccg gcg agg gcc ggc gtg tcc    1968
Ser Pro Ser Pro Ala Val Ser Ser Val Pro Ala Arg Ala Gly Val Ser
            645             650             655

atc gcg cac ctg cca atg ttc gcc gcg tgg acc gac gca tga           2010
Ile Ala His Leu Pro Met Phe Ala Ala Trp Thr Asp Ala
            660             665
```

<210> 9
<211> 669
<212> PRT
<213> Oryza sativa

<400> 9
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Met Ala Ser Gly Asn Ser Ser Ser Ser Ser Gly Ser Met Ala Ala Thr
  1               5              10              15

Ala Gly Gly Val Gly Gly Trp Leu Gly Phe Ser Leu Ser Pro His Met
            20              25              30

Ala Thr Tyr Cys Ala Gly Gly Val Asp Asp Val Gly His His His His
            35              40              45

His His Val His Gln His Gln Gln Gln His Gly Gly Gly Leu Phe Tyr
        50              55              60

Asn Pro Ala Ala Val Ala Ser Ser Phe Tyr Tyr Gly Gly Gly His Asp
65              70              75              80

Ala Val Val Thr Ser Ala Ala Gly Gly Gly Ser Tyr Tyr Gly Ala Gly
                85              90              95
```

Phe Ser Ser Met Pro Leu Lys Ser Asp Gly Ser Leu Cys Ile Met Glu
        100   105   110

Ala Leu Arg Gly Gly Asp Gln Glu Gln Gln Gly Val Val Val Ser Ala
        115   120   125

Ser Pro Lys Leu Glu Asp Phe Leu Gly Ala Gly Pro Ala Met Ala Leu
        130   135   140

Ser Leu Asp Asn Ser Ala Phe Tyr Tyr Gly Gly His Gly His His Gln
145   150   155   160

Gly His Ala Gln Asp Gly Gly Ala Val Gly Gly Asp Pro His His Gly
                165   170   175

Gly Gly Gly Phe Leu Gln Cys Ala Val Ile Pro Gly Ala Gly Ala Gly
                180   185   190

His Asp Ala Ala Leu Val His Asp Gln Ser Ala Ala Ala Val Ala Ala
        195   200   205

Gly Trp Ala Ala Met His Gly Gly Gly Tyr Asp Ile Ala Asn Ala Ala
        210   215   220

Ala Asp Asp Val Cys Ala Ala Gly Pro Ile Ile Pro Thr Gly Gly His
225   230   235   240

Leu His Pro Leu Thr Leu Ser Met Ser Ser Ala Gly Ser Gln Ser Ser
                245   250   255

Cys Val Thr Val Gln Ala Ala Ala Gly Glu Pro Tyr Met Ala Met
                260   265   270

Asp Ala Val Ser Lys Lys Arg Gly Gly Ala Asp Arg Ala Gly Gln Lys
        275   280   285

Gln Pro Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser
        290   295   300

Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala
305   310   315   320

His Leu Trp Asp Asn Ser Cys Lys Lys Glu Gly Gln Thr Arg Lys Gly
                325   330   335

Arg Gln Val Tyr Leu Gly Gly Tyr Asp Met Glu Glu Lys Ala Ala Arg
                340   345   350

Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr His Ile
        355   360   365

Asn Phe Pro Leu Glu Asp Tyr Gln Glu Glu Leu Glu Glu Met Lys Asn
        370   375   380

Met Ser Arg Gln Glu Tyr Val Ala His Leu Arg Arg Lys Ser Ser Gly
385   390   395   400

Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln
        405   410   415

His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ser Gly Asn Lys Asp
        420   425   430

Leu Tyr Leu Gly Thr Phe Ile Ala Ser Ala Phe Ala Ala Ala Arg Arg
        435   440   445

Ala Arg His Ala Gly Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val
    450   455   460

Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile
465   470   475   480

Thr Arg Tyr Asp Val Asp Lys Ile Leu Glu Ser Ser Thr Leu Leu Pro
            485   490   495

Gly Glu Leu Ala Arg Arg Lys Gly Lys Val Gly Asp Gly Gly Gly Ala
        500   505   510

Ala Ala Val Ala Asp Ala Ala Ala Ala Leu Val Gln Ala Gly Asn Val
        515   520   525

Ala Glu Trp Lys Met Ala Thr Ala Ala Ala Leu Pro Ala Ala Ala Arg
    530   535   540

Thr Glu Gln Gln Gln Gln His Gly His Gly Gly His Gln His His Asp
545   550   555   560

Leu Leu Pro Ser Asp Ala Phe Ser Val Leu Gln Asp Ile Val Ser Thr
            565   570   575

Val Asp Ala Ala Gly Ala Pro Pro Arg Ala Pro His Met Ser Met Ala
        580   585   590

Ala Thr Ser Leu Gly Asn Ser Arg Glu Gln Ser Pro Asp Arg Gly Val
    595   600   605

Gly Gly Gly Gly Gly Gly Gly Val Leu Ala Thr Leu Phe Ala Lys Pro
    610   615   620

Ala Ala Ala Ser Lys Leu Tyr Ser Pro Val Pro Leu Asn Thr Trp Ala
625   630   635   640

Ser Pro Ser Pro Ala Val Ser Ser Val Pro Ala Arg Ala Gly Val Ser
            645   650   655

Ile Ala His Leu Pro Met Phe Ala Ala Trp Thr Asp Ala
        660   665

<400> 10
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catcaccagc acgggcggtg gcaggcgcgc atcggccgcg tctcgggcaa caaggacctc 120
tacctgggaa cgttcagcac gcaggaggag gccgcggagg cgtacgacgt ggccgcgatc 180
aagttccgcg gcctcagcgc ggtcaccaac ttcgacatca cgcggtacga cgtggacaag 240
atcatggaga gcagcacgct gctcccgggc gagcaggtcc ggcgcaggaa ggaaggcgcc 300
gacgccgcgg tctcggaggc cgccgccgcg ctggtgcagg ccggcaactg catgacggac 360
acctggaaga tccaggcggc tctgccagct gccgcgcggg ccgacgagcg cggcgccggc 420
cagcagcagc gccaggactt gctgtcgagc gaggccttct cgctgctcca cgacatcgtg 480
tccgtcgacg ctgctgctgg tacaggaca gggacagggg gcatgtcgaa cgcgtcgtcg 540
tcgctggccc ccagcgtgag caactcccgg gagcagagcc cggaccgggg cggcgccagc 600
ctcgccatgc tcttcgccaa gcccgtcgcg gcgcccaagc tggcttgccc gctgccgctg 660
gggtcgtggg tgtcgccgtc cgcggtgtcc gccaggccgc ccggcgtgtc aatcgcgcac 720
ctgccggtgt cgccgcgtg gaccgacgca tgaacaaaca tccgtgtcat taccagggta 780
tggttctttt ggtttgctta gagcgtgctt tttagctggg taaggttagc tgcgtagcgg 840
tgatctgatc agcatatgtg agaggaacta gccatgcgtg tctgctttgt cctcctgcga 900
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ttcatcaatg agctgggatt cagacctcaa aaaaaaaaa aaaaaaaaa aaaaaaa 1137

<210> 11
<211> 585
<212> PRT
<213> Gossypium hirsutum

<400> 11
Met Ser Asn Trp Leu Gly Phe Ser Leu Thr Pro Asp Leu Arg Ile Asp
 1   5   10   15

Glu Ser Phe Gly Arg Glu Asp His Gly Gly Phe Pro Ser Val Met Pro
            20   25   30

Leu Arg Ser Asp Gly Ser Leu Cys Val Val Asp Pro Phe Arg Arg Ser
        35   40   45

Ser Ile Ala Ala Asp Glu Asp Trp Arg Tyr Glu Asn Gly Ile Gly Ser
    50   55   60

Ala Thr Ala Asn Glu Gln Gly Pro Lys Leu Glu Asp Phe Leu Gly Cys
65   70   75   80

Tyr Ser Asn Ser Pro Ser Gln Glu Thr Lys Ala Tyr Cys Gly Thr His
                85   90   95

Glu Asn Gln Asn Thr Val Pro Ser Pro Thr Arg Ile Asn Val Asn Val
            100   105   110

Ala Pro Asn Tyr Ser Ser Ser Gly Asp Ala Glu Ala Ala Glu Asn Phe
        115   120   125

Thr Asn Pro Ser Ser Phe Ile Gln Thr Tyr Arg Asn Tyr Asn Glu Asn
    130   135   140

Pro Gln Thr Leu Met Ala Gly Gly His Ser Leu Gln Gln Cys Asp Pro
145   150   155   160

Asn Pro Asn His Asn Gln Arg Ser Gly Val His His Val Pro Phe Glu
            165   170   175

Ser Ala Thr Ser Val Ser Gly Phe Lys Ser Trp Leu Arg Gln Thr Pro
           180   185   190

Phe Pro Gly Gly Lys Ala Ser Gly Asn Glu Thr Asn Asn Asn Phe Asn
      195   200   205

Phe Gln Ala Leu Ser Leu Thr Met Ser Pro Thr Ser Arg Asn Gly Phe
    210   215   220

Pro Ala Ile Ala Pro Leu Glu Val Val Asp Asn Arg Lys Arg Pro Val
225   230   235   240

Gly Lys Asn Leu Thr Arg Glu Ser Val Pro Arg Lys Ser Ile Asp Thr
           245   250   255

Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp
         260   265   270

Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Lys Glu
         275   280   285

Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys
    290   295   300

Glu Glu Lys Ala Ala Lys Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
305   310   315   320

Gly Pro Thr Thr His Ile Asn Phe Pro Leu Ser Thr Tyr Glu Lys Glu
           325   330   335

Leu Glu Glu Met Lys Asn Met Thr Arg Gln Glu Phe Val Ala His Leu
         340   345   350

Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Val Tyr Arg Gly
         355   360   365

Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
      370   375   380

Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu
385   390   395   400

Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Thr
           405   410   415

Ser Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val Lys Arg Ile
         420   425   430

Cys Ser Ser Ser Thr Leu Ile Gly Gly Glu Leu Ala Lys Arg Ser Pro
         435   440   445

Lys Asp Thr Ala Ser Ile Ala Pro Glu Asp Tyr Asn Ser Cys Ala Ser
    450   455   460

Ser Ala Ser Pro Gln Pro Leu Leu Ala Ile Pro Ser Gly Glu Ala Ser
465   470   475   480

Asp Glu Leu Ala Asp Met Val Trp Thr Ala Asn Ser Asp Glu Gln Gln
               485   490   495

Gln His Gln Ser Thr Asn Thr Asn Asn Asp Ala Ser Leu Ala Asn Ser
                500   505   510

Ser Ser Arg Asn Ser Ser Asn Pro Gln Ser Pro Lys Gly Ser Ile Gly
         515   520   525

Leu Ala Ser Asp Lys Phe Gly Ile Gly Gly Asp Tyr Ser His His Gly
         530   535   540

Tyr Phe Ser Leu Lys Gly Ser Lys Tyr Glu Asp Gly Asn Ser Glu Thr
545   550   555   560

Asp Asn Ser Asn Glu Asn Arg Leu Gly Asn Leu Gly Leu Val His Lys
               565   570   575

Ile Pro Met Phe Ala Leu Trp Asn Glu
         580   585

<210> 12
<211> 1137
<212> DNA
<213> Zea mays

<400> 12
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tacctgggaa cgttcagcac gcaggaggag gccgcggagg cgtacgacgt ggccgcgatc 180
aagttccgcg gcctcagcgc ggtcaccaac ttcgacatca cgcggtacga cgtggacaag 240
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gacgccgcgg tctcggaggc cgccgccgcg ctggtgcagg ccggcaactg catgacggac 360
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cagcagcagc gccaggactt gctgtcgagc gaggccttct cgctgctcca cgacatcgtg 480
tccgtcgacg ctgctgctgg tacagggaca gggacagggg gcatgtcgaa cgcgtcgtcg 540
tcgctggccc ccagcgtgag caactcccgg gagcagagcc cggaccgggg cggcgccagc 600
ctcgccatgc tcttcgccaa gcccgtcgcg gcgcccaagc tggcttgccc gctgccgctg 660
gggtcgtggg tgtcgccgtc cgcggtgtcc gccaggccgc ccggcgtgtc aatcgcgcac 720
ctgccggtgt cgccgcgtg gaccgacgca tgaacaaaca tccgtgtcat taccagggta 780
tggttctttt ggtttgctta gagcgtgctt tttagctggg taaggttagc tgcgtagcgg 840
tgatctgatc agcatatgtg agaggaacta gccatgcgtg tctgctttgt cctcctgcga 900
ttcctcctcc agttgcgttg cgaggaggtt tcttttttgta ataccggggc tagatagcac 960
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<210> 13
<211> 255
<212> PRT
<213> Zea mays

<400> 13
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Arg Pro Thr Arg Pro Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly
 1               5                  10                  15

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp
             20                  25                  30

Gln Ala Arg Ile Gly Arg Val Ser Gly Asn Lys Asp Leu Tyr Leu Gly
         35                  40                  45

Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala
     50                  55                  60

Ile Lys Phe Arg Gly Leu Ser Ala Val Thr Asn Phe Asp Ile Thr Arg
 65              70                  75                      80

Tyr Asp Val Asp Lys Ile Met Glu Ser Ser Thr Leu Leu Pro Gly Glu
                 85                  90                  95

Gln Val Arg Arg Arg Lys Glu Gly Ala Asp Ala Ala Val Ser Glu Ala
         100                 105                 110

Ala Ala Ala Leu Val Gln Ala Gly Asn Cys Met Thr Asp Thr Trp Lys
         115                 120                 125

Ile Gln Ala Ala Leu Pro Ala Ala Ala Arg Ala Asp Glu Arg Gly Ala
     130             135                 140

Gly Gln Gln Gln Arg Gln Asp Leu Leu Ser Ser Glu Ala Phe Ser Leu
145             150                 155                 160

Leu His Asp Ile Val Ser Val Asp Ala Ala Ala Gly Thr Gly Thr Gly
             165                 170                 175

Thr Gly Gly Met Ser Asn Ala Ser Ser Ser Leu Ala Pro Ser Val Ser
             180                 185                 190

Asn Ser Arg Glu Gln Ser Pro Asp Arg Gly Gly Ala Ser Leu Ala Met
     195                 200                 205

Leu Phe Ala Lys Pro Val Ala Ala Pro Lys Leu Ala Cys Pro Leu Pro
     210                 215                 220

Leu Gly Ser Trp Val Ser Pro Ser Ala Val Ser Ala Arg Pro Pro Gly
225             230                 235                 240

Val Ser Ile Ala His Leu Pro Val Phe Ala Ala Trp Thr Asp Ala
             245                 250                 255
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<210> 14
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

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<400> 14
cgcggcgaat tcatgaagtc tttttgtgat aatg                         34


<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 15
cgcggcgtcg acgaatcagc ccaagcagc                               29


<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 16
cgcggcccat ggatgaagcg cataaatgag a                            31


<210> 17
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 17
cgcggcctcg aggtatcagt ccaagaagca a                            31


<210> 18
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 18
cgcggcccat ggaatgaaga gtatggaaaa tgatg                        35
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<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 19
cgcggcctcg aggcatctgt ccaagctgca                                30


<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 20
caacgttcgt caagttcaat gc                                        22


<210> 21
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 21
tgccataata ctcgaactca gtagga                                    26


<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 22
tcagtttcat tgcgcacaca ccagaa                                    26


<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 23
gagcgtgtgc atggttggtg                                              20


<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 24
ctcgaggcat ctgtccaggc tgcaaaaac                                    29


<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (1)
<223> Gly, Ala, Val, Leu or Ile

<400> 25
Xaa Ser Ser Ser Arg Glu
  1               5


<210> 26
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (1)
<223> Gly, Ala, Val, Leu or Ile

<400> 26
Xaa Ser Asn Ser Arg Glu
  i               5
```

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<210> 27
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     peptide

<400> 27
Asn Ser Ser Ser Arg Asn
 1                   5



<210> 28
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     peptide

<220>
<221> MOD_RES
<222> (4)
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> (7)
<223> Gly, Ala, Val, Leu or Ile

<400> 28
Ser Ser Leu Xaa Thr Ser Xaa Ser Ser Ser Arg Glu
 1                   5                   10



<210> 29
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     peptide

<220>
<221> MOD_RES
<222> (4)
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> (7)
<223> Gly, Ala, Val, Leu or Ile
```

<400> 29
Ser Ser Leu Xaa Pro Ser Xaa Ser Asn Ser Arg Glu
 1   5.   10

<210> 30
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (4)
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> (7)
<223> Gly, Ala, Val, Leu or Ile

<400> 30
Ser Ser Leu Xaa Thr Ser Xaa Ser Asn Ser Arg Glu
 1   5   10

<210> 31
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (3)
<223> Gly, Ala, Val, Leu or Ile

<400> 31
Ser Leu Xaa Asn Ser Ser Ser Arg Asn
 1   5

<210> 32
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 32
ggcgcgccac aatggccagc ggcggcggca g   31

<210> 33
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide

<400> 33
cctgcaggtc aggcatctgt ccaggctgca a   31

<210> 34
<211> 555
<212> PRT
<213> Arabidopsis thaliana

<400> 34
Met Lys Ser Phe Cys Asp Asn Asp Asp Asn Asn His Ser Asn Thr Thr
 1   5   10   15

Asn Leu Leu Gly Phe Ser Leu Ser Ser Asn Met Met Lys Met Gly Gly
            20   25   30

Arg Gly Gly Arg Glu Ala Ile Tyr Ser Ser Ser Thr Ser Ser Ala Ala
        35   40   45

Thr Ser Ser Ser Ser Val Pro Pro Gln Leu Val Val Gly Asp Asn Thr
    50   55   60

Ser Asn Phe Gly Val Cys Tyr Gly Ser Asn Pro Asn Gly Gly Ile Tyr
65   70   75   80

Ser His Met Ser Val Met Pro Leu Arg Ser Asp Gly Ser Leu Cys Leu
                85   90   95

Met Glu Ala Leu Asn Arg Ser Ser His Ser Asn His His Gln Asp Ser
            100   105   110

Ser Pro Lys Val Glu Asp Phe Phe Gly Thr His His Asn Asn Thr Ser
            115   120   125

His Lys Glu Ala Met Asp Leu Ser Leu Asp Ser Leu Phe Tyr Asn Thr
        130   135   140

Thr His Glu Pro Asn Thr Thr Thr Asn Phe Gln Glu Phe Phe Ser Phe
145   150   155   160

Pro Gln Thr Arg Asn His Glu Glu Glu Thr Arg Asn Tyr Gly Asn Asp
                165   170   175

Pro Ser Leu Thr His Gly Gly Ser Phe Asn Val Gly Val Tyr Gly Glu
            180   185   190

Phe Gln Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser
     195   200   205

Cys Ile Thr Gly Ser His His His Gln Gln Asn Gln Asn Gln Asn His
     210   215   220

Gln Ser Gln Asn His Gln Gln Ile Ser Glu Ala Leu Val Glu Thr Ser
225   230   235   240

Val Gly Phe Glu Thr Thr Thr Met Ala Ala Ala Lys Lys Lys Arg Gly
          245   250   255

Gln Glu Asp Val Val Val Val Gly Gln Lys Gln Ile Val His Arg Lys
          260   265   270

Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr
          275   280   285

Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
     290   295   300

Phe Lys Lys Glu Gly His Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly
305   310   315   320

Gly Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala
          325   330   335

Leu Lys Tyr Trp Gly Pro Ser Thr His Thr Asn Phe Ser Ala Glu Asn
          340   345   350

Tyr Gln Lys Glu Ile Glu Asp Met Lys Asn Met Thr Arg Gln Glu Tyr
     355   360   365

Val Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser
     370   375   380

Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala
385   390   395   400

Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe
          405   410   415

Gly Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys
          420   425   430

Phe Arg Gly Thr Asn Ala Val Thr Asn Phe Asp Ile Thr Arg Tyr Asp
          435   440   445

Val Asp Arg Ile Met Ser Ser Asn Thr Leu Leu Ser Gly Glu Leu Ala
     450   455   460

Arg Arg Asn Asn Asn Ser Ile Val Val Arg Asn Thr Glu Asp Gln Thr
465   470   475   480

Ala Leu Asn Ala Val Val Glu Gly Gly Ser Asn Lys Glu Val Ser Thr
          485   490   495

```
Pro Glu Arg Leu Leu Ser Phe Pro Ala Ile Phe Ala Leu Pro Gln Val
            500                 505                 510

Asn Gln Lys Met Phe Gly Ser Asn Met Gly Gly Asn Met Ser Pro Trp
            515                 520                 525

Thr Ser Asn Pro Asn Ala Glu Leu Lys Thr Val Ala Leu Thr Leu Pro
        530                 535                 540

Gln Met Pro Val Phe Ala Ala Trp Ala Asp Ser
545                 550                 555
```

```
<210> 35
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 35
Leu Gly Phe Ser Leu Ser
  1               5


<210> 36
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 36
Leu Gly Phe Ser Leu Thr
  1               5


<210> 37
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 37
Met Pro Leu Lys Ser Asp Gly Ser
  1               5
```

```
<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 38
Met Pro Leu Arg Ser Asp Gly Ser
  1               5


<210> 39
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 39
Met Pro Ile Lys Ser Asp Gly Ser
  1               5


<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 40
Pro Lys Leu Glu Asp Phe
  1               5


<210> 41
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 41
Pro Lys Val Glu Asp Phe
  1               5
```

<210> 42
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 42
Asp Tyr Lys Asp Asp Asp Lys
  1   5